

FIG. I

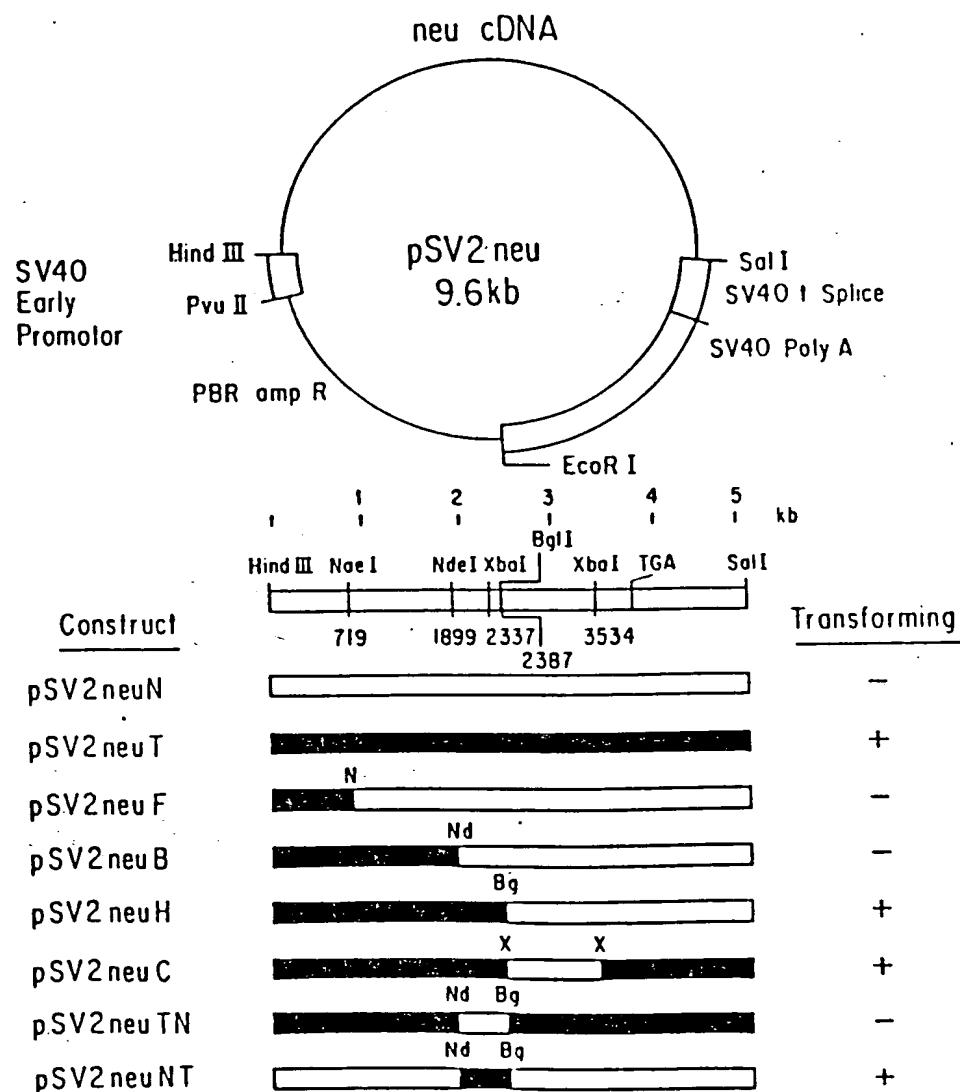
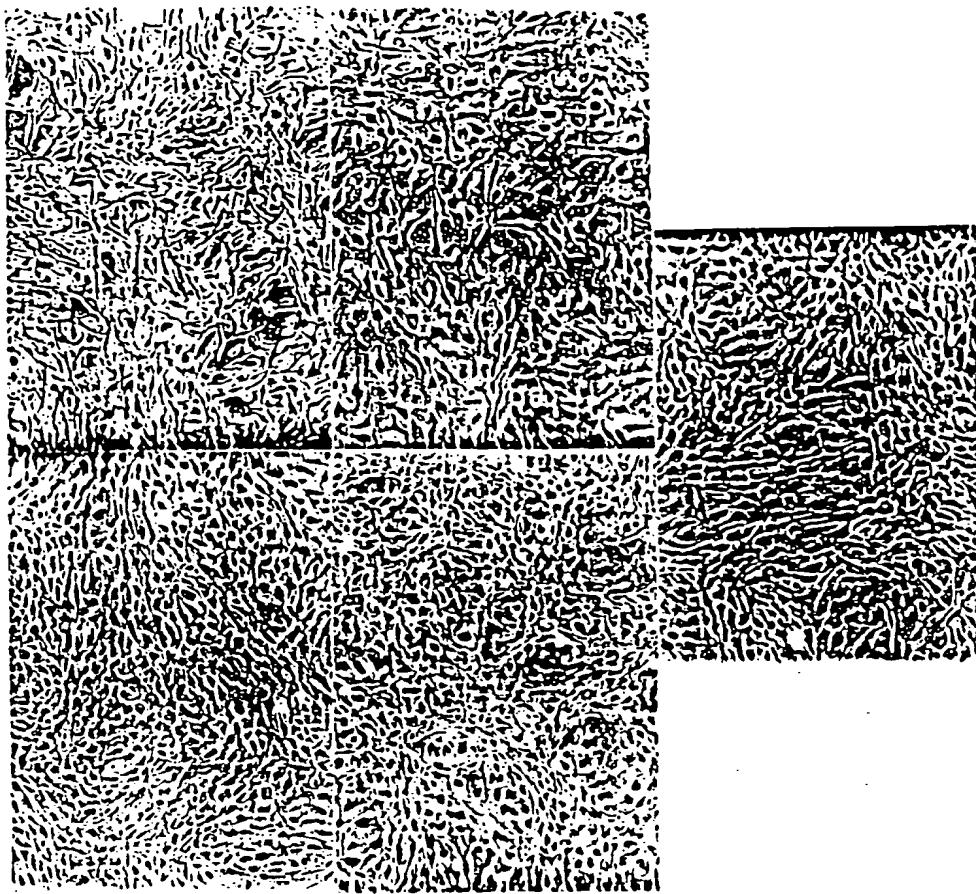
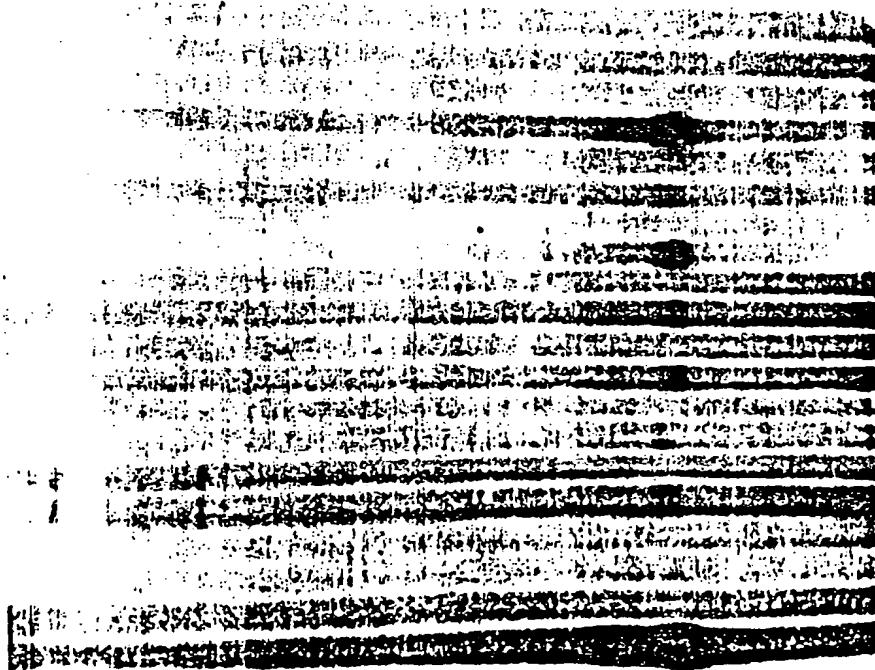


FIG.2A



p 185 —

FIG.2B



a b c d e f g h i j
- + - + - + - + - + - + - +

FIG.3

normal

| | | | | | | | | | | | | | | | | | |
|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|
| glu | gln | arg | ala | ser | pro | val | thr | phe | ile | ile | ala | thr | val | : | gly | val | aa 666 |
| GAG | CAG | AGA | GCC | AGC | CCG | GTG | ACA | TTC | ATC | ATT | GCA | ACT | GTA | : | GGC | GTC | |
| transforming | | | | | | | | | | | | | | CAG | | | |
| | | | | | | | | | | | | | | glu | | | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|
| leu | leu | phe | leu | ile | leu | val | val | val | val | gly | ile | leu | ile | lys | arg | arg | aa 683 |
| CTG | CTG | TTC | CTG | ATC | TTA | GTG | GTG | GTC | GTC | GTT | GGA | ATC | CTA | ATC | AAA | CGA | AGG |

FIG.4

A) ACGCCCAC TACAGTTGCAAT nucleotides 1999-2018, wild-type sequence

 *

B) ACGCCCTCTACAGTTGCAAT nucleotides 999-2018, T₂₀₁₂ to A

C) CCGTCCTCAGCTGTGACC nucleotides 996-1013, control probe

 *

D) ACGCCCCCTACAGTTGCAAT nucleotides 1999-2018, T₂₀₁₂ to G

FIG.5

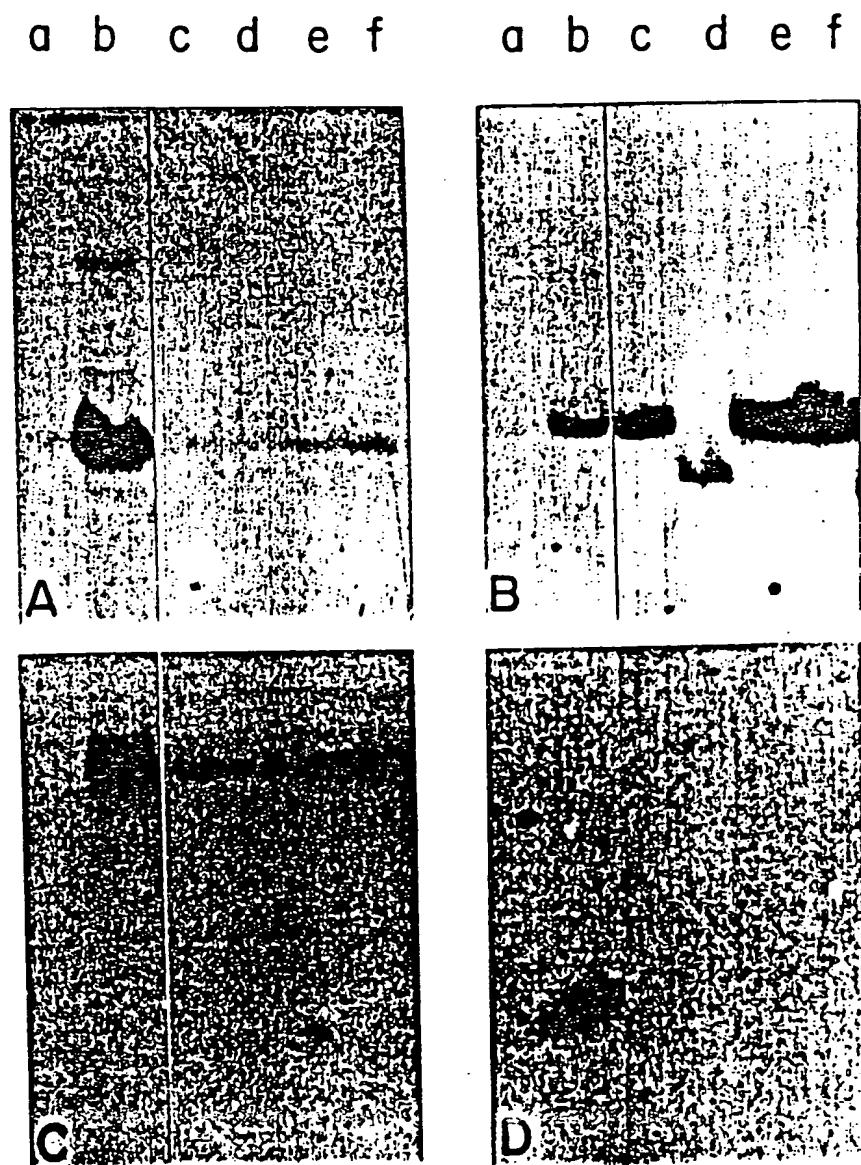


FIG. 6

a b c d e f g h i j

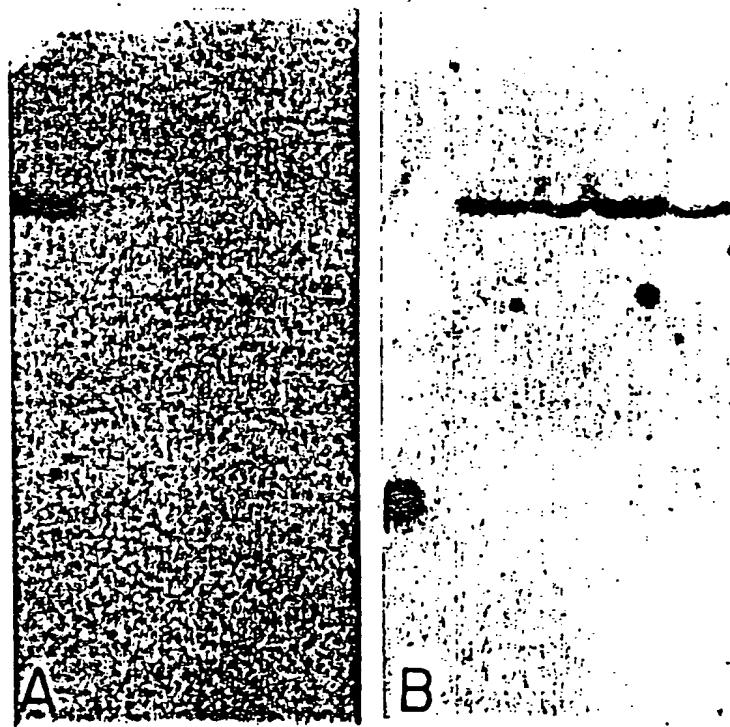
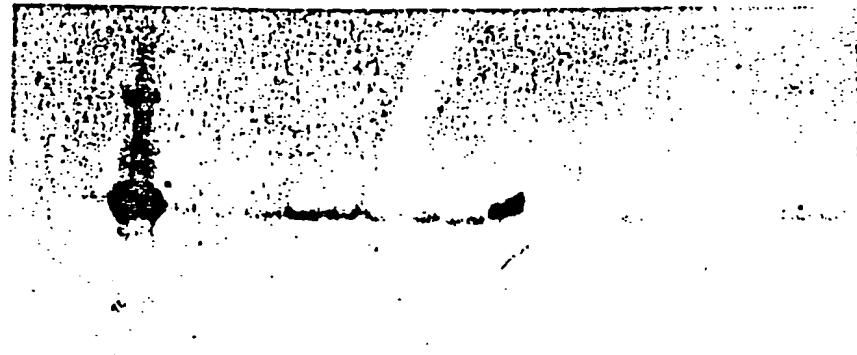
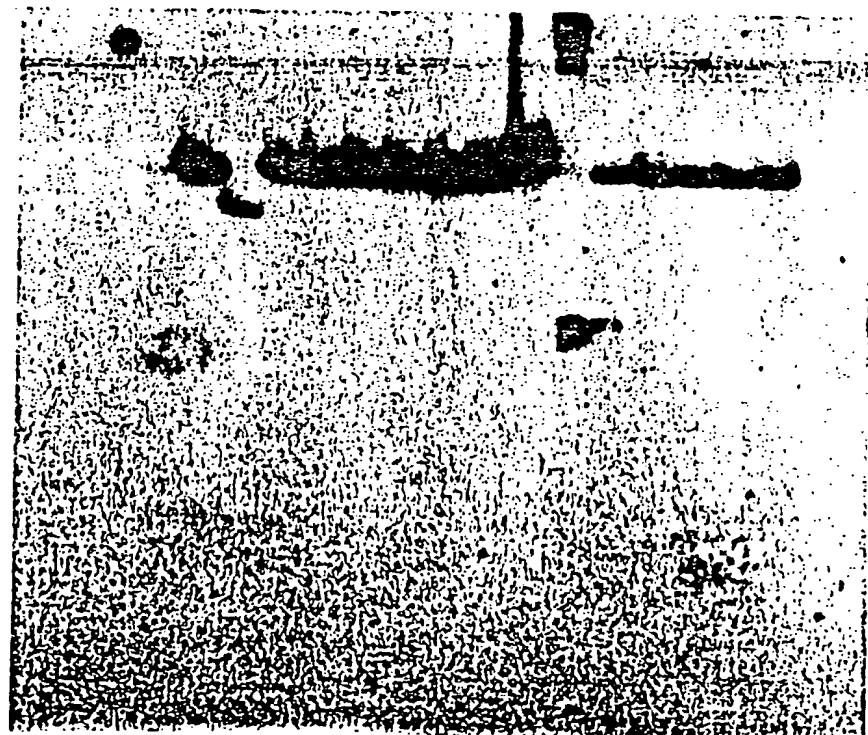


FIG.7

N G B 1 2 3 4 5 6 7 8 9 10 11 12 13 14 c1 c2



N G B 1 2 3 4 5 6 7 8 9 10 11 12 13 14 c1 c2



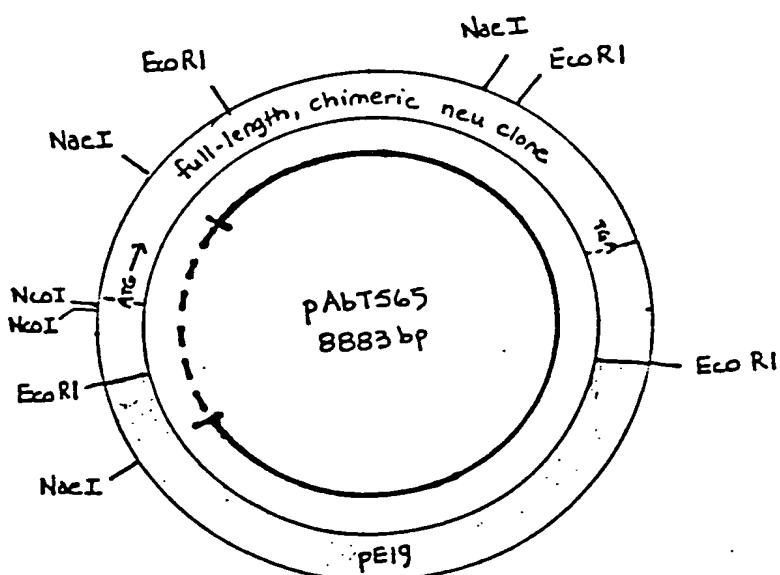
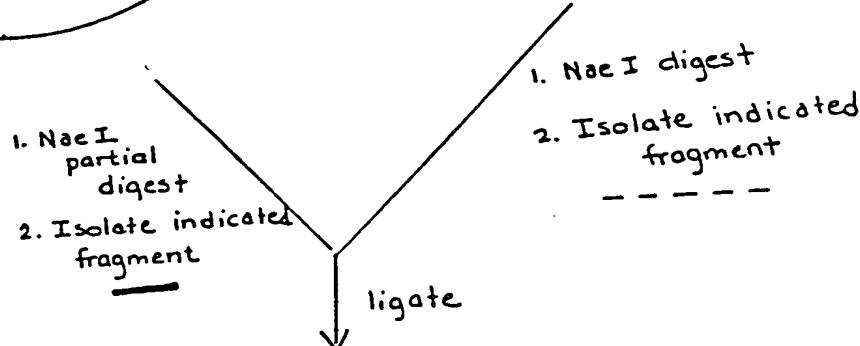
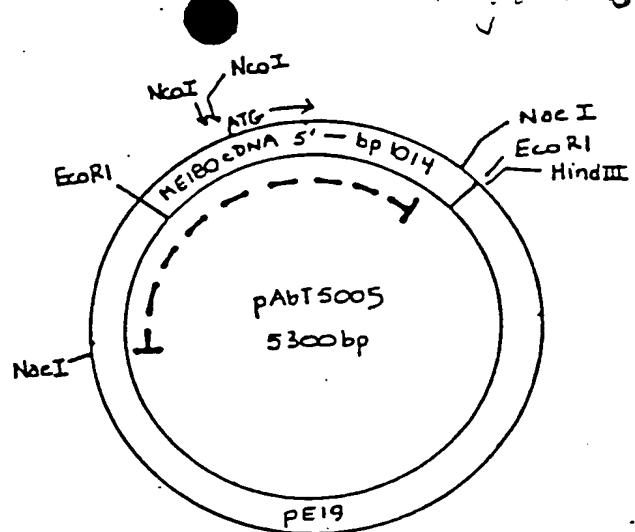
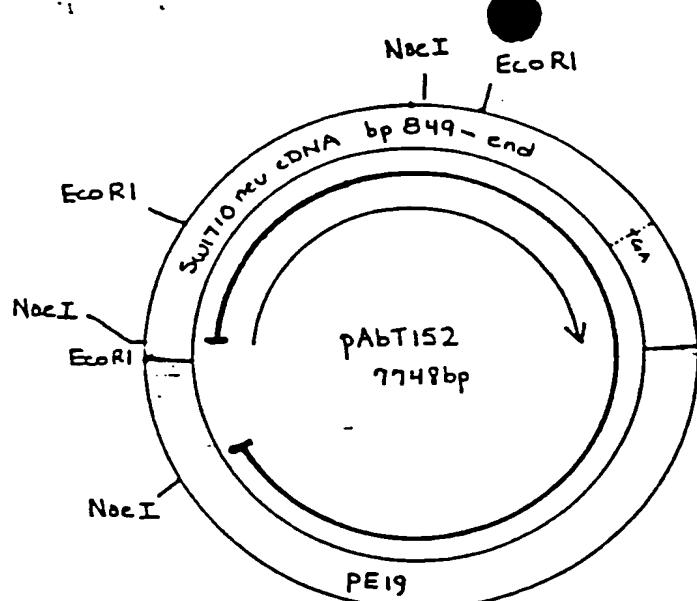


Fig 11. Construction of full length neu cDNA clone from ME180 and SW1710 neu cDNAs

Construction of pMax neu

Figure 9

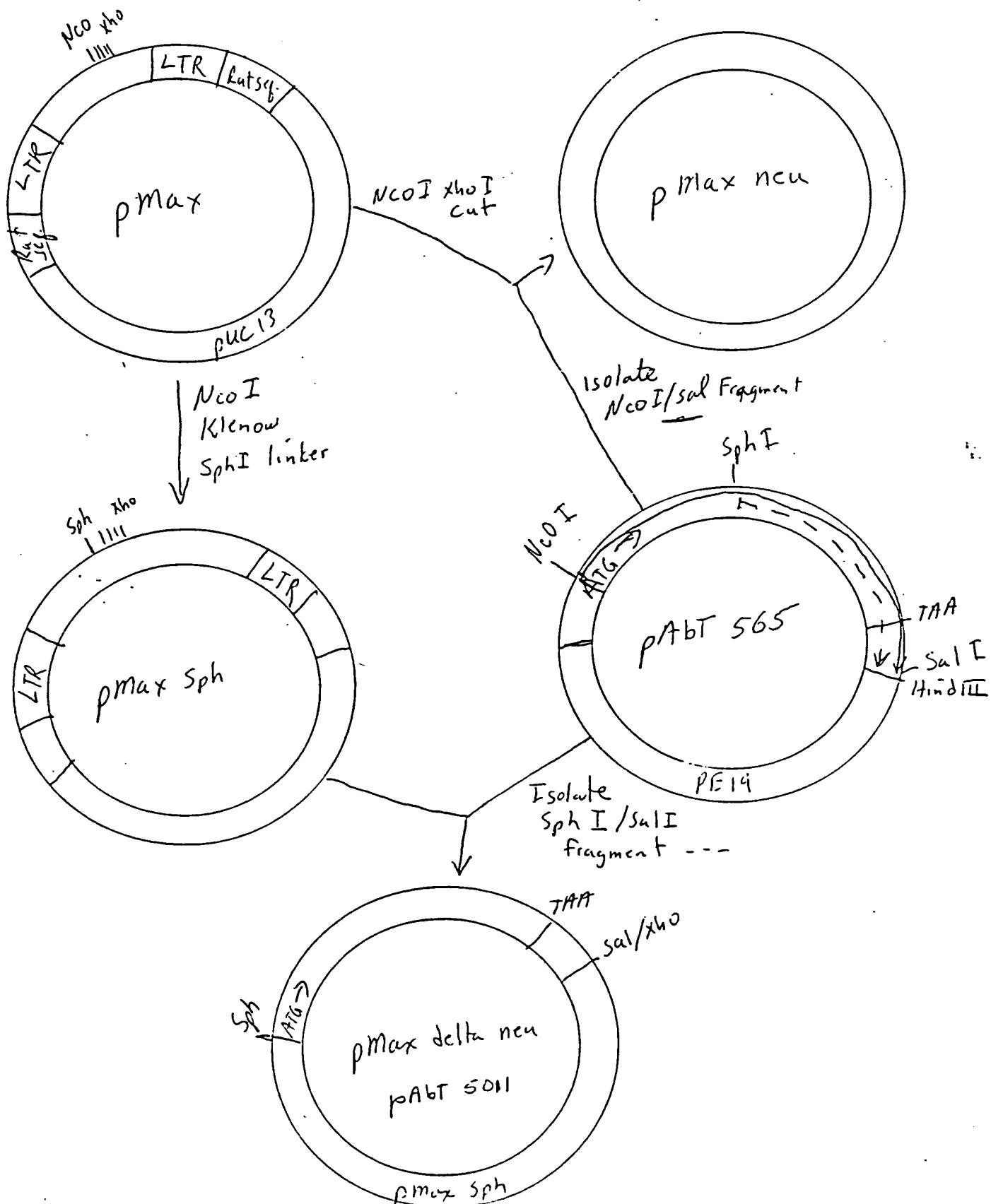


Figure 114
Neu Oncogene Probe Design:

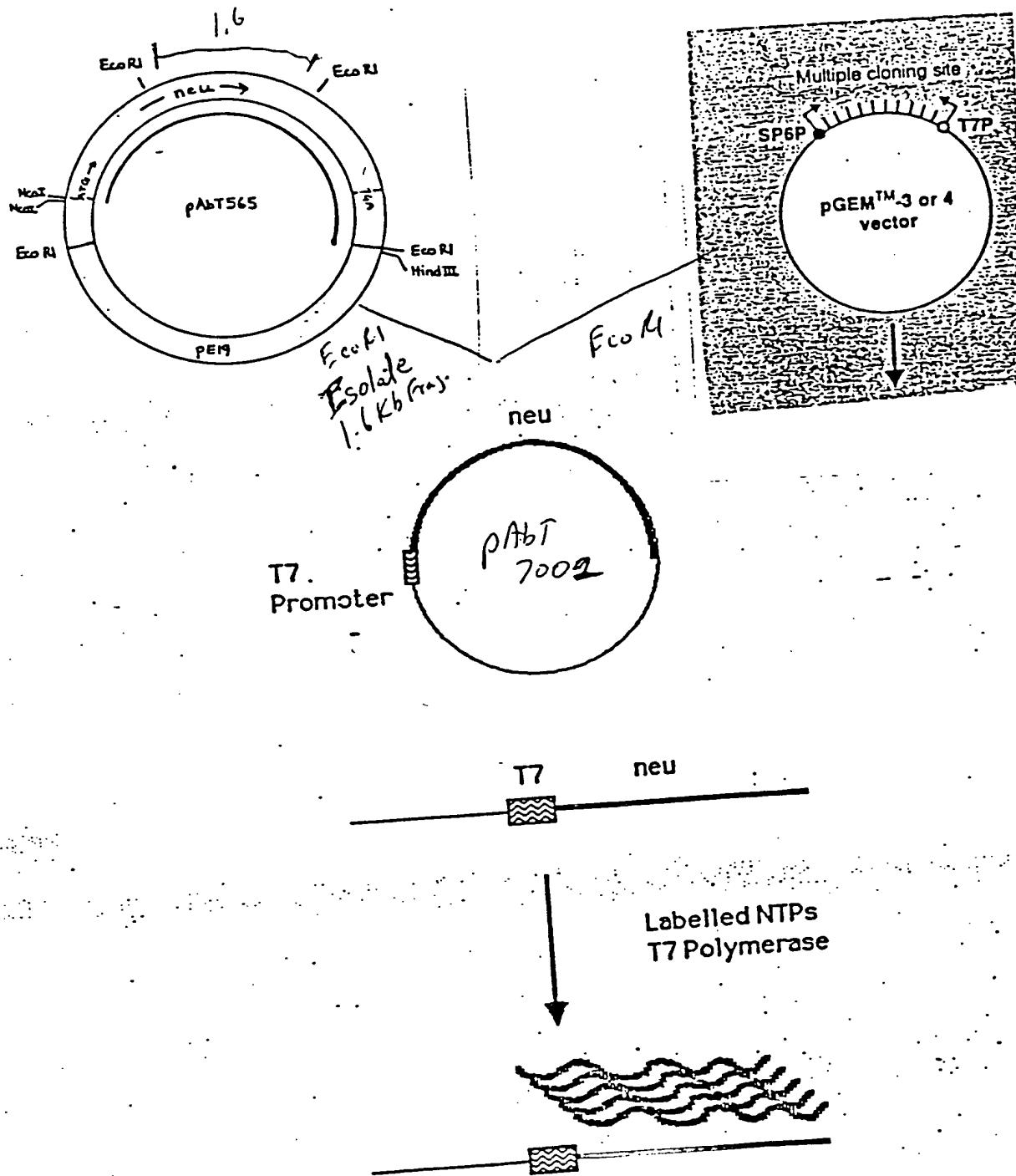
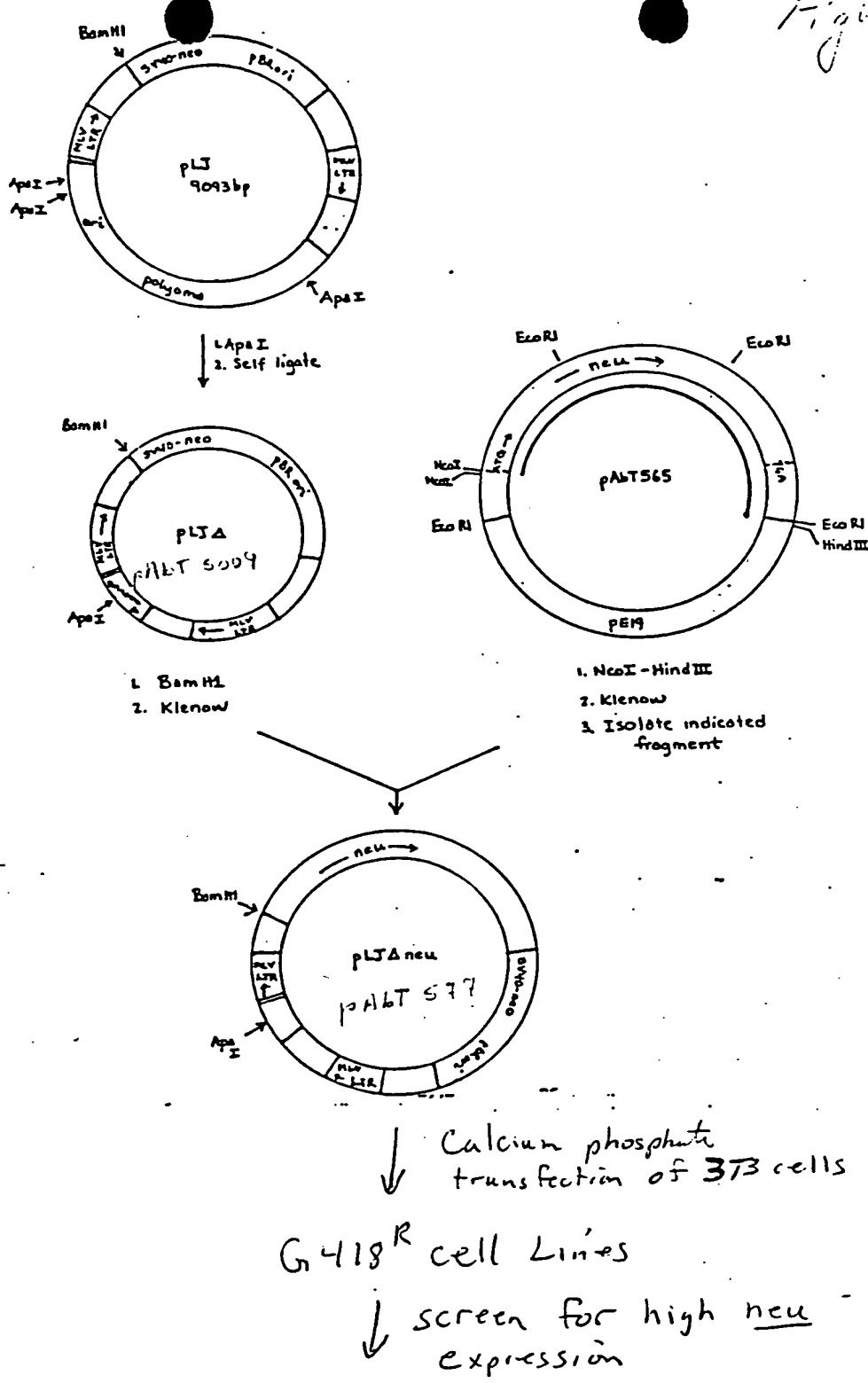


Figure 11



18-3-7